

GenCore version 4.5
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OM protein - protein search, using sw model

Run on:

September 4, 2002, 16:16:08 ; Search time 172.18 Seconds

(without alignments)
51.241 Million cell updates/sec

Title: US-09-052-089a-6
perfect score: 293

Sequence: 1 LSLCTICSDFFDHSRDVAI.....IOWFETAPSRTCPQCRIQVG 51

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SPTRMBL19:
1: sp_archea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvirus:
16: sp_bacteriap:
17: sp_archeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	293	100.0	470	11 Q08854
2	286	97.6	223	11 Q922MB
3	286	97.6	469	4 Q9bfW2
4	286	97.6	470	11 Q9CPP4
5	272	92.8	469	4 Q00467
6	244	83.3	433	13 Q9YGN2
7	128	43.7	435	5 Q95SS5
8	128	43.7	455	5 Q9v8D7
9	127	43.3	310	10 Q82372
10	127	43.3	420	4 Q75866
11	125	42.7	325	10 Q9M9U7
12	124.5	42.5	263	5 Q95RB5
13	123	42.0	158	5 Q92ZS4
14	115	39.2	327	11 Q9DAH2
15	39.2	349	10 Q947X9	0947x9 oryza sativ
16	38.9	1181	5 097260	plasmidium

RESULT	1	PRELIMINARY;	PRT;	470 AA.
ID	008854			
AC	008854;			
DT	01-JUL-1997 (TREMBLrel. 04, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	MTRIP.			
GN	TRAIP OR MTRIP.			
OS	MUS musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID:10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97258620; PubMed=9104814;			
RA	Lee S.Y., Lee S.Y., Choi Y.,			
RT	"TRAF-interacting protein (TRIP): a novel component of the tumor necrosis factor receptor (TNFR) and CD30-TRAF signaling complexes that inhibits TRAF2-mediated NF-κB activation.";			
RT	J. EXP. MED. 185:1275-1285(1997). CC -SIMILARITY: CONTAINS 1 ZINC FINGER. EMBL: U77844; AAB2994; -.			
DR	MGI: MGI:1096377; Traip.			
DR	InterPro: IPR001841; Znf_ring.			
DR	PFAM: PF00097; zf-C3HC4; 1.			
DR	SMART: SM00184; RING; 1.			
KW	Zinc-finger.			
SEQUENCE	470 AA; 53191 MW; 00FD705B52645133 CRC64;			
Query	Match	100.0%; Score 293; DB 11; Length 470;		
Best Local Similarity	100.0%; Pred. No. 3.7e-31;			
Matches	51; Conservativeness 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 LSLCTICSDFFDHSRDVAIHCQHFLQCIOWFETAPSRTCPQCRIQVG 51			
Db	4 LSCTICSDFFDHSRDVAIHCQHFLQCIOWFETAPSRTCPQCRIQVG 54			

DR	Pfam; PR0097; zf-C3HC4; 1.	Stapleton M., Brokstein P., Hong L., Agbonyani A., Carlson J., Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., KW Zinc-finger; SM00184; RING; 1.
KW	SEQUENCE; 469 AA;	Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
SO	Best local similarity 96.0%; Score 272; DB 4; Length 469; Matches 48; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	DR EMBL; AY060610; AAL28158.1; -.
Db	5 ALCTICSDPFDFHSRDAVANHGHTPHQCLIQWFETAPSRTPCPCRQV 51	DR SEQUENCE; 435 AA; A48455 MW; OBFFOAC81DBD9416E CRC64;
RESULT	6	Query Match 92.8%; Score 272; DB 4; Length 469;保守性 1; 错配 1; 插入 0; 缺失 0; 空隙 0;
ID	09VG2	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
AC	09VG2;	匹配数 48; 保守性氨基酸 1; 错配氨基酸 1; 插入氨基酸 0; 缺失氨基酸 0; 空隙氨基酸 0;
DT	01-MAY-1999 (TREMBLrel. 10, Created)	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
DE	TRAF. INTERACTING PROTEIN.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
GN	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
OS	Euarayota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes; Tetraodontidae; Takifugu.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
OC	[1]; NCBI_TaxID=31033;	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RN	SEQUENCE FROM N.A.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RX	MEDLINE-99148833; PubMed=10025966;	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Cottage A.J., Clark M., Hawker K., Umrania Y., Wheller D., Bishop M., Elgar G.; "Three receptor genes for plasminogen related growth factors in the genome of the puffer fish Fugu rubripes.";	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RT	FEBS Lett. 443:370-374(1999). -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RL	EMBL; A010131; CA09094; 1; -.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
DR	InterPro; IPR001841; Znf_ring.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
DR	Pfam; PR0097; zf-C3HC4; 1.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
DR	SMART; SM00184; RING; 1; NCBI_TaxID=31033;	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
KW	Zinc-finger.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
SQ	SEQUENCE 433 AA; 49201 MW; A8C31AAA4216E8C2 CRC64;	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
Query Match	83.3%; Score 244; DB 13; Length 433; Best Local Similarity 83.0%; Pred. NO. 1.28-24; Matches 39; Conservative 6; Mismatches 2; Indels 0; Gaps 0; Oligo 0;	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
QY	4 CTICSDFFDFHSRDAVANHGHTPHQCLIQWFETAPSRTPCPCRQV 50	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
Db	7 CTICSDFFDFHSRDAVANHGHTPHQCLIQWFETAPSRTPCPCRQV 53	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RESULT	7	Query Match 83.3%; Score 244; DB 13; Length 433; Best Local Similarity 83.0%; Pred. NO. 1.28-24; Matches 39; Conservative 6; Mismatches 2; Indels 0; Gaps 0; Oligo 0;
Q9SS5	PR0097; PRELIMINARY; PRT; 435 AA.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
ID	09SS5	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
AC	09SS5	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
DT	01-DEC-2001 (TREMBLrel. 19, Created)	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
DE	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
GN	CG5140.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
OS	Drosophila melanogaster (Fruit fly).	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Endopterygota; Drosophilidae; Drosophila.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RN	{1}; NCBI_TaxID=7227;	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RP	SEQUENCE FROM N.A.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Strain-BERKELEY; MEDLINE-2019006; PubMed=10731132;	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RX	Adams M.D., Celiniere S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandao R.C., Rogers Y.H., Bazelé R.G., Chame M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Heitj G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D., Balley R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S., Borikova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busan D.A., Butler H., Cadieu E., Centter A., Chandra I., Cherry J.M., Cawley S., Dahake C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dotson K., Douc L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ihbegam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai C.D., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Mosher J.A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.R., Nixon K., Nuskeen D.R., Pacieb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Snee B.C., Stidham-Kiamos I., Simpson M., Skupski M.P., Smith T., Snue R.C., Spiller E., Spradling A.C., Stapleton M., Strong R., Sun E., Svartkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.-H., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., Strain-N.A., STRAIN-Y, CN BN SP;	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Stapleton M., Brokstein P., Hong L., Agbonyani A., Carlson J., Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Stapleton M., Brokstein P., Hong L., Agbonyani A., Carlson J., Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K., RA Yu C., Lewis S.E., Rubin G.M., Celinder S., RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	最佳局部相似度 96.0%; 预测号. 2.4e-28; 错配 1; 插入 0; 缺失 0; 空隙 0;
RA	Champre M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J.,	

RT	"The genome sequence of <i>Drosophila melanogaster</i> .";	RESULT 10
RL	Science 287:2185-2195(2000).	ID 075866 PRELIMINARY; PRT; 420 AA.
CC	-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.	ID 075866 PRELIMINARY; PRT; 420 AA.
DR	EMBL; AE003800; AAF57730; 1; -	ID 075866 PRELIMINARY; PRT; 420 AA.
DR	FLYBase; FBgn0031314; CG5540.	ID 075866 PRELIMINARY; PRT; 420 AA.
DR	InterPro; IPR01841; zf-C3HC4; 1.	ID 075866 PRELIMINARY; PRT; 420 AA.
DR	Pfam; PF00097; zf-C3HC4; 1.	ID 075866 PRELIMINARY; PRT; 420 AA.
DR	SMART; SM00184; RING; 1.	ID 075866 PRELIMINARY; PRT; 420 AA.
KW	Zinc-finger	ID 075866 PRELIMINARY; PRT; 420 AA.
SQ	SEQUENCE 455 AA; 50726 MW; BEA74F4CAC8EFD5B CRC64;	ID 075866 PRELIMINARY; PRT; 420 AA.
Query Match	43.7%; Score 128; DB 5; Length 455;	Best Local Similarity 50.0%; Pred. No. 4e-09;
Matches	22; Conservative 6; Mismatches 14; Indels 2; Gaps 1;	Pred. No. 4e-09; Best Local Similarity 50.0%; Pred. No. 4e-09;
Qy	4 CTICSDFFDHSRDAVATHCIGHFTFHLCIQLQWFETAPSRCPOCR 47	Db 6 CVICAELFGQADEVFATVCGHMFHHNCLNQWLDR- SKTCPOCR 47
Db	01-NOV-1998 (TREMBLrel. 08, Created)	01-NOV-1998 (TREMBLrel. 08, Created)
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)	01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	AT2G28840 PROTEIN.	AT2G28840 PROTEIN.
GN	Arabidopsis thaliana (Mouse-ear cress).	Arabidopsis thaliana (Mouse-ear cress).
OS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.	eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX	NCBI_TaxID=3702;	NCBI_TaxID=3702;
RN	[1]	[1]
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	STRAIN=CV. COLUMBIA;	STRAIN=CV. COLUMBIA;
RX	MEDLINE=20083487; PubMed=10617197;	MEDLINE=20083487; PubMed=10617197;
RA	Lin X., Kaul S., Rounseley S.D., Shea T.P., Benito M.-I., Town C.D.,	Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Fieldlyum T.V.,
RA	Bueli C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,	Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA	Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,	Adams D., Niezman W.C., White O., Eisen J.A.,
RA	Copeland G.P., Preuss D., Salzberg S.L., Fraser C.M., Venter J.C.,	Salzberg S.L., Fraser C.M., Venter J.C.,
RA	"sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.", 761-768(1999).	"sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.", 761-768(1999).
RT	Nature 402:761-768(1999).	Nature 402:761-768(1999).
RN	[2]	[2]
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	STRAIN=CV. COLUMBIA;	STRAIN=CV. COLUMBIA;
RA	Lin X.:	Lin X.:
RA	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RL	-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.	-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR	EMBL; AC003496; AAC35217; 1; -	EMBL; AC003496; AAC35217; 1; -
DR	HSSP; P2890; 1; CIRC.	HSSP; P2890; 1; CIRC.
DR	InterPro; IPR0101841; Znf_ring.	InterPro; IPR0101841; Znf_ring.
DR	Pfam; PF00097; zf-C3HC4; 1.	Pfam; PF00097; zf-C3HC4; 1.
DR	SMART; SM00184; RING; 1.	SMART; SM00184; RING; 1.
KW	Zinc-finger	Zinc-finger
SQ	SEQUENCE 310 AA; 35390 MW; EEEC1401152F5E2C CRC64;	SEQUENCE 310 AA; 35390 MW; EEEC1401152F5E2C CRC64;
Query Match	43.3%; Score 127; DB 10; Length 310;	Best Local Similarity 41.7%; Pred. No. 4e-09;
Best Local Similarity	41.7%; Pred. No. 4e-09;	Best Local Similarity 41.7%; Pred. No. 4e-09;
Matches	20; Conservative 11; Mismatches 15; Indels 2; Gaps 1;	Matches 20; Conservative 11; Mismatches 15; Indels 2; Gaps 1;
Qy	3 LCTICSDFFDHSRDAVATHCIGHFTFHLCIQLQWFETAPSRCPOCR 50	3 LCTICSDFFDHSRDAVATHCIGHFTFHLCIQLQWFETAPSRCPOCR 50
Db	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DT	01-OCT-2000 (TREMBLrel. 15, Created)	01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)	01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE	F6A1.12 PROTEIN.	F6A1.12 PROTEIN.
GN	Arabidopsis thaliana (Mouse-ear cress).	Arabidopsis thaliana (Mouse-ear cress).
OS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.	eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX	NCBI_TaxID=3702;	NCBI_TaxID=3702;
RN	[1]	[1]
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RA	Federer Spiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,	Federer Spiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA	Altafai H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,	Altafai H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,
RA	Gonzalez A., Kremenetskskaia I., Kim C., Lenz C., Li J., Liu S.,	Gonzalez A., Kremenetskskaia I., Kim C., Lenz C., Li J., Liu S.,
RA	Luros S., Schwartz J.K., Shinn P., Toriumi M., Vysotskiaia V.S.,	Luros S., Schwartz J.K., Shinn P., Toriumi M., Vysotskiaia V.S.,
RA	Walker M., Yu G., Becker J., Theologis A., Davis R.W.,	Walker M., Yu G., Becker J., Theologis A., Davis R.W.,
RA	Submitted JAN-2000 to the EMBL/GenBank/DDBJ databases.	Submitted JAN-2000 to the EMBL/GenBank/DDBJ databases.
CC	-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.	-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR	AC011809; AAFT7102; 1; -	AC011809; AAFT7102; 1; -
DR	InterPro; IPR01661; IF;	InterPro; IPR01661; IF;

RN [2]	SEQUENCE OF 65-344 FROM N.A.	AC Q9LMT3;
RP	Rose M., Hempel S., Entian K.-D., Mewes H.W., Lemcke K., Mayer K.F.X.;	DT 01-CCT-2000 (TREMBLrel. 15, Created)
RA	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.	DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
RL	[3]	DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
RN	SEQUENCE FROM N.A.	DE F2H15.19 PROTEIN.
RP	Vandenbol M., Jallet C., Portetelle D., Mewes H.W., Lemcke K., Mayer K.F.X.;	GN F2H15.19
RA	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.	OS Arabidopsis thaliana (Mouse-ear cress).
RL	[4]	OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; euksids II; Brassicales; Brassicaceae; Arabidopsis.
RN	SEQUENCE FROM N.A.	OC euksids II
RP	EU Arabidopsis sequencing project;	OX NEB1-TAXID=3702;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.	RN [1]
CC	-! - SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.	RP SEQUENCE FROM N.A.
DR	EMBL; AL02223; CAI18230.1; -	RC STRAIN=EV_COLUMBIA;
DR	EMBL; AL161565; CB79495.1; -	RA Sakano H., Liu S.X., Etgu P., Lee J.M., Lenz C., Pham P., Toriumi M., Yu G., Chan A., Chung M., Goldsmith A., Liu A., Smith A., Vaysberg M., Altafi H., Brooks S., Bueler E., Chao Q., Conn L., Conway A.B., Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B., Mirzani M., Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R., Federer N.A., Theologis A.;
DR	InterPro; IPR001841; zf-C3HC4; 1.	RT "The sequence from BAC F2H15 from Arabidopsis thaliana chromosome 1.;" Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR	SMART; SM00184; RING; 1.	DR EMBL; PR00097; zf-C3HC4; 1.
KW	Hypothetical protein; Zinc-finger.	DR InterPro; IPR01841; zf-ring.
SQ	SEQUENCE 344 AA; 38720 MW; EB31D0BF5EDAF700 CRC64;	DR PR00097; zf-C3HC4; 1.
Query Match	Best local Similarity 38.2%; Score 112; DB 10; Length 344; Matches 18; Conservative 9; Mismatches 16; Indels 2; Gaps 1;	DR SMART; SM00184; RING; 1.
Qy	4 CTICSDFFDHRSRVAATHGHTPHLQLQWFETAPSRTCPQCRIQV 50	DR Q9LMT3; PRELIMINARY; PRT; 368 AA.
Db	229 CSICLDDDKGSKAKEMCKHKHRCIVPWLHSS--CPYCRYEL 273	DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
RESULT 21		DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
Q94L9		DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
ID Q94L9	PRELIMINARY;	DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
AC		DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
DT	01-DEC-2001 (TREMBLrel. 19, Created)	DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)	DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
DE	ATR1G7970/F2H15.16.	DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
OS	Arabidopsis thaliana (Mouse-ear cress);	DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.	DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
OC	euksids II	DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
NCBI_TAXID=3702;		DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
RN	[1]	DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
RP	SEQUENCE FROM N.A.	DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
RA	Cheek R., Chen H., Kim C.J., Koesema E., Meyers M.C., Bahn J., Bowser L., Carninci P., Date J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;	DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
RT	"Arabidopsis" CDNA clones.;" Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.	DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
DR	EMBL; AL0428290; AL161622.1; -	DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
SQ	SEQUENCE 368 AA; 41618 MW; 79AD4BB0790A08E CRC64;	DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
Query Match	Best local Similarity 36.4%; Score 112; DB 10; Length 383; Matches 16; Conservative 11; Mismatches 15; Indels 2; Gaps 1;	DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
Qy	4 CTICSDFFDHRSRVAATHGHTPHLQLQWFETAPSRTCPQCRIQV 47	DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
Db	335 CSICQDEVEREDEVGEVLNGGHSPFHVCVKOWL--SRKNACPVCK 376	DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
RESULT 23		DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
Q9Y9TB		DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
ID Q9Y9TB	PRELIMINARY;	DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
AC		DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
DT	01-MAY-2000 (TREMBLrel. 13, Created)	DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
DE	CG11737 PROTEIN.	DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
DR	CG11737.	DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
OS	Drosophila melanogaster (Fruit fly).	DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; OC Prierygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; OC Ephydriidea; Drosophilidae; Drosophila.	DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
OC	NCBI_TAXID=227;	DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
RN	[1]	DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
RP	SEQUENCE FROM N.A.	DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
RC	STRAIN=BERKELEY;	DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
RX	MEDLINE=20196006; Pubmed=10731132;	DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.
RA	Adams M.D., Celinkiner S.E., Holt R.A., Evans C.A., Gocayne J.D., Admanatides P.G., Schefer S.E., Li P.W., Hoskins R.A., Gallo R.F., Adams M.D., Celinkiner S.E., Holt R.A., Evans C.A., Gocayne J.D., Admanatides P.G., Schefer S.E., Li P.W., Hoskins R.A., Gallo R.F., Amarnath S.E., Richards S., Ashburner M., Henderson S.N., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.H., Blazej R.G., Champé M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews P., Frankish C., Baldwin D., Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolstakov S., Borikova D., Botchtein M.R., Bouck H., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler J., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Fablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doupe J.E., Downes M., Duran-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,	DR Q9Y9TB; PRELIMINARY; PRT; 621 AA.

Fosler C.,	Gabrielian A.E.,	Garg N.S.,	Gelbart W.M.,	Glasser K.,	RA
Glodek A.,	Gong F.,	Correll J.H.,	Gu Z.,	Guan P.,	Harris M.,
Harris N.L.,	Harvey D.,	Heiman T.J.,	Hernandez J.R.,	Houck J.,	RA
Hostett D.,	Houston K.A.,	Howland T.J.,	Wei M.-H.,	Ibegwam C.,	RA
Jalali M.,	Kalush F.,	Karpfen G.H.,	Ke Z.,	Kennison J.A.,	Ketchum K.A.,
Kimmel B.E.,	Kodira C.D.,	Kraft C.,	Kravitz S.,	Kulp D.,	Lai Z.,
Lasko P.,	Lei Y.,	Levitsky A.A.,	Li D.,	Li Z.,	Liang Y.,
Liu X.,	Matrei B.,	McIntosh T.C.,	McLeod M.P.,	McPherson D.,	RA
Merkulov G.,	Milshina N.V.,	Mobarry C.,	Morris J.,	Moschrefi A.,	RA
Mount S.M.,	Moy M.,	Murphy B.,	Muzny D.M.,	Nelson D.L.,	RA
Nelson D.R.,	Nelson K.A.,	Nixon K.,	Nusskern D.R.,	Pacleb J.M.,	RA
Palazzolo M.,	Pittman G.S.,	Pan S.,	Pollard J.,	Puri V.,	Reese M.G.,
Reinert K.,	Remington K.,	Saunders R.D.C.,	Scheeler F.,	Shen H.,	RA
Shue B.C.,	Sidén-Kiamos I.,	Simpson M.,	Skupski M.P.,	Smith T.,	RA
Spieler E.,	Spradling A.C.,	Stapleton M.,	Strong R.,	Sun E.,	RA
Svirskas R.,	Tector C.,	Turner R.,	Venter R.,	Wang A.H.,	Wang X.,
Wang Z.-Y.,	Wasserman D.A.,	Weinstock G.M.,	Weissenbach J.,	Wu D.,	Yao Q.A.,
Williams S.M.,	Woodage T.,	Worley K.C.,	Xiang G.,	Zhao Q.,	Zheng L.,
Ye J.,	Yeh R.-F.,	Zaveri J.S.,	Zhan H.,	Zhu X.,	Smith H.O.,
Zhang X.H.,	Zhong F.N.,	Zhong W.,	Zhou X.,	Zhu S.,	Smith H.O.,
Gibbs R.A.,	Mers E.W.,	Rubin G.M.,	Venter J.C.,	Wang X.,	RA
RT	"The genome sequence of <i>Drosophila melanogaster</i> ,";	RA	RA	RA	RA
RL	Science 287:2185-2195(2000)	RA	RA	RA	RA
CC	-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.	RA	RA	RA	RA
DR	EMBL; AE003779; AAFF5196.1; -.	RA	RA	RA	RA
DR	FlyBase; FBgn0039875; CG1937.	RA	RA	RA	RA
DR	InterPro; IPR001841; Znf_fring.	RA	RA	RA	RA
DR	PFAM; PF00097; zf-C3HC4; 1.	RA	RA	RA	RA
DR	SMART; SM00184; RING; 1.	RA	RA	RA	RA
KW	Zinc-finger.	RA	RA	RA	RA
SQ	SEQUENCE 621 AA; 68752 MW; A8D6EB160952C0A1 CRC64;	RA	RA	RA	RA
RESULT 24					
Q55SP2	PRELIMINARY;	PRTR;	626 AA.		
ID Q55SP2;					
AC					
DT 01-DEC-2001 (TREMBLER. 19, Created)					
DT 01-DEC-2001 (TREMBLER. 19, Last sequence update)					
DT 01-DEC-2001 (TREMBLER. 19, Last annotation update)					
DE GH1117P.					
GN CG1937.					
OS Drosophila melanogaster (Fruit fly).					
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;					
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;					
OC Ephydriidae; Drosophilidae; Drosophila.					
OX NC_01_TAXID=7227;					
[1] SEQUENCE FROM N.A.					
RC STRAIN=N, CN BW SP;					
RA Stapleton M., Brobststein P., Hong L., Agbayani A., Carlson J.,					
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,					
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,					
RA Nuncio J., Paclib J., Paragas V., Park S., Phouanenavong S., Wan K.,					
RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.					
DR EMBL; AE060677; AAL2825.1; -.					
SQ SEQUENCE 626 AA; 6872 MW; F881B88D51B724EC CRC4;					
Query Match 38.2%; Score 112; DB 5; Length 626;					
Best Local Similarity 40.0%; Pred. No. 8.3e-07;					
Matches 20; Conservative 9; Mismatches 15; Indels 6; Gaps 3;					
RESULT 25					
Q9LTUB	PRELIMINARY;	PRTR;	325 AA.		
ID Q9LTUB;					
AC					
DT 01-OCT-2000 (TREMBLER. 15, Created)					
DT 01-OCT-2000 (TREMBLER. 15, Last sequence update)					
DT 01-DEC-2001 (TREMBLER. 19, Last annotation update)					
DE GB2A27103.1.					
OS Arabidopsis thaliana (Mouse-ear cress).					
RA Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
RA Spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae;					
RA eurosids II; Brassicales; Brassicaceae; Arabidopsis.					
RA NCBI_TAXID=3702;					
RA [1]					
RA SEQUENCE FROM N.A.					
RC STRAIN=COLUMBIA;					
RA MEDLINE=20277480; PubMed=10819329;					
RA SATO S., NAKAMURA Y., KANEKO T., KATO T., ASAMIZU E., TABATA S.;					
RA RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.					
RA RN [2]					
RA RP SEQUENCE FROM N.A.					
RC STRAIN=COLUMBIA;					
RA MEDLINE=20277480; PubMed=10819329;					
RA SATO S., NAKAMURA Y., KANEKO T., KATO T., ASAMIZU E., TABATA S.;					
RA RT "Structural analysis of <i>Arabidopsis thaliana</i> chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty Pl and TAC RT clones";					
RT DNA Res. 7:131-135(2000).					
RA CL -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.					
RA DR EMBL; AB024334; BAB02789.1; -.					
RA DR RSSP; P28990; 1ICHC.					
RA DR InterPro; IPR001841; Znf_fring.					
DR Pfam; PF00097; zf-C3HC4; 1.					
DR SMART; SM00184; RING; 1.					
KW Zinc-finger.					
SQ SEQUENCE 325 AA; 36432 MW; 694044F361053DE4 CRC64;					
Query Match 37.9%; Score 111; DB 10; Length 325;					
Best Local Similarity 40.4%; Pred. No. 5.9e-07;					
Matches 19; Conservative 10; Mismatches 16; Indels 2; Gaps 2;					
Q9LZ10	PRELIMINARY;	PRTR;	274 AA.		
ID Q9LZ10					
AC					
DT 01-OCT-2000 (TREMBLER. 15, Created)					
DT 01-OCT-2000 (TREMBLER. 15, Last sequence update)					
DT 01-DEC-2001 (TREMBLER. 19, Last annotation update)					
DE HYPOTHETICAL_31.1_KDA PROTEIN.					
GN F9G14_60.					
OS Arabidopsis thaliana (Mouse-ear cress).					
RA Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
RA Spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae;					
RA eurosids II; Brassicales; Brassicaceae; Arabidopsis.					
RA NCBI_TAXID=3702;					
RA [1]					
RA SEQUENCE FROM N.A.					
RC Beran M., Tierry N., Ardiles W., Buysshaert C., Daesselle R.,					
RA De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,					
RA Villaruel R., Gielens J., Van Montagu M., Bancroft I., Mewes H.W.,					
RA Rudd S., Lemcke K., Mayer K.F.X.,					
RA Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.					
RA RN [1]					

Query Match	36.5%	Score 107; DB 13;	Length 923;	RP
Best Local Similarity	38.3%	Pred. No. 5.7e-06;	RA	
Matches	18;	Conservative 7;	RA	
		Mismatches 20;	RL	
OY	4	CTICSDFFDHRSRDVAIHCGHTEFLQCLLWFETAPSRTCPORIQV 50	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.	
Db	871	CTICUSILEEGEDVVRLLPCNHLFHOCVCDWLIT--NKKCPICRVDI 915	"-SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.	
DR		DR Interpro: IPR001841; znf_ring.	DR	
DR		PFam: PF0097; zf_C3HC4_1.	DR	
DR		SMART: SM00184; RING; 1.	DR	
KW		Zinc-finger.	KW	
SQ		SEQUENCE 506 AA; 56518 MW; 1B06751A4E299FE8 CRC64;	SQ	
RESULT	34			
Q99ML9		PRELIMINARY; ID 999M9	PRT; 989 AA.	
AC	Q99ML9;	ID 01-JUN-2001 (TREMBREL. 17, Created)		
DT	01-JUN-2001 (TREMBREL. 17, Last sequence update)			
DT	01-DEC-2001 (TREMBREL. 19, Last annotation update)			
DE	ARKADIA.			
GN	ARK OR ARKADIA.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi.			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
NCBI_TaxID	100900;			
RN	[1]	SEQUENCE FROM N.A.		
RP		STRAIN=129/SV;		
RC		MEDLINE=21195971; PubMed=11298452;		
RA		Episkopou V., Arkell R., Timmons P.M., Walsh J.J., Andrew R.L., Swan D.,		
RA		"Induction of the mammalian node requires Arkadia function in the extraembryonic lineages."		
Nature	410:825-830(2001).			
RT		-- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.		
DR		EMBL: AF330191; AXN38272.1; -.		
DR		MGB; MGI:1934919; Ark.		
DR		Interpro: IPR001211; PLP_A2.		
DR		Interpro: IPR001841; Znf_fing.		
DR		SMART; SM00184; RING; 1.		
DR		PROSITE; PS00118; PA2_HIS; UNKNOWN.1.		
SQ		SEQUENCE 989 AA; 107896 MW; 212E3C37BC70DCBS CRC64;		
Query Match	36.5%	Score 107; DB 11;	Length 989;	
Best Local Similarity	38.3%	Pred. No. 6.1e-06;		
Matches	18;	Conservative 7;		
Matches	18;	Mismatches 20;		
Indels	2;	Gaps 1;		
QY	4	CTICSDFFDHRSRDVAIHCGHTEFLQCLLWFETAPSRTCPORIQV 50		
Db	937	CTICLSILEEGEDVVRLLPCNHLFHOCVCDWLIT--NKKCPICRVDI 981		
RESULT	35			
Q9ML43		PRELIMINARY; ID 09ML43	PRT; 506 AA.	
AC	Q9ML43;	ID 01-OCT-2000 (TREMBREL. 15, Created)		
DT	01-OCT-2000 (TREMBREL. 15, Last sequence update)			
DT	01-DEC-2001 (TREMBREL. 19, Last annotation update)			
DE	PUTATIVE RING ZINC FINGER PROTEIN.			
GN	Arabidopsis thaliana (Mouse-ear cress).			
OS	Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; euroids II; Brassicales; Brassicaceae; Arabidopsis.			
OC	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; euroids II; Brassicales; Brassicaceae; Arabidopsis.			
NCBI_TaxID	3702;			
RN	[1]	SEQUENCE FROM N.A.		
RP		STRAIN=CY - COLUMBIA;		
RC		MEDLINE=21016719; PubMed=11130712;		
RA		Theologis A., Ecker J.R., Palm C.J., Fedderspiel N.A., Kaul S., Buehler E., Chan A., Chao Q., Chen H., Cirkut R.F., Chin C.W., Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K., Dunn P., Egwu T., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y., Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hulizar L., Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E., Kim C.J., Koo H.L., Kremenetskaya I., Kurtz D.B., Kwan A., Langin-Hooper S., Lee J.M., Lenz C.A., Li J.H., Li Y.-P., Liu X., Liu S.X., Liu Z.A., Luos J.S., Maiti R., Marziali A., Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I., Pal G., Peeler J., Pham P.K., Rizzo M., Rooney T., Rowley D., Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M., Sun H., Taillon L.J., Tambang G., Toriumi M.J., Town C.D., Utterback T., Van Aken S., Vayberg M., Venter J.C., Davis R.W., Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;		
RA		Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;		
RT		Sequence and analysis of chromosome 1 of the plant Arabidopsis thaliana.		
RL		Nature 408:816-820(2000).		
CC		-- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.		
DR		Interpro: IPR001841; Znf_ring.		
DR		PFam: PF0097; zf_C3HC4_1.		
DR		SMART; SM00184; RING; 1.		
KW		SEQUENCE 367 AA; 40616 MW; 6114F620CF2AD4A9 CRC64;		
Query Match	36.2%	Score 106; DB 10;	Length 367;	
Best Local Similarity	36.4%	Pred. No. 3.1e-06;		
Matches	16;	Conservative 8;		
Indels	2;	Gaps 1;		
OY	4	CTICSDFFDHRSRDVAIHCGHTEFLQCLLWFETAPSRTCPORIQV 47		
RA		Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.		
RA		Mayr K.F.X.; Stonkewig T., Stumpf J., Mewes H.W., Lemcke K., Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.		

Db	319	CICQDEYEAKDVEGELRCGHFRHDCVQOWL--VRKNSCPVCOK	360	OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae; OC euroids II; Brassicales; Brassicaceae; Arabidopsis; OX NCBI_TaxID=3702;
RESULT	37			
ID	P90990	PRELIMINARY;	PRT;	425 AA.
AC	P90990			
DT	01-MAY-1997	(TREMBREL. 03, Created)		
DT	01-DEC-2001	(TREMBREL. 19, Last sequence update)		
DE	01-DEC-2001	(TREMBREL. 19, Last annotation update)		
DE	B0432.9	PROTEIN.		
GN	B0432.9			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;			
OC	Rhabdiidae; Peloderinae; Caenorhabditis.			
OX	NCBI_TAXID=6239;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BRISTOL N2;			
RX	MEDLINE=94150718; PubMed=7960398;			
RA	Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,			
RA	Bonfield J., Burton J., Cornell M., Copsey T., Cooper J., Fulton L.,			
RA	Craxton M., Dear S., Du Z., Durbin R., Evelo A., Fulton L.,			
RA	Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,			
RA	Kershaw J., Kirstein J., Latreille P.,			
RA	Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,			
RA	Parsons J., Percy C., Rifkin L., Roopa A., Saunders D., Shownkeen R.,			
RA	Smaldon N., Smith A., Sonnemann E., Staden R., Sulston J.,			
RA	Tillyer-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,			
RA	Watson A., Weinstock L., Wilkinson-Spratt J., Wohldmann P.,			
RT	"2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans";			
RL	Nature 368:32-38(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BRISTOL N2;			
RA	Henkhaus J., Wohldmann P.;			
RT	"The sequence of <i>C. elegans</i> cosmid B0432.;"			
RL	Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BRISTOL N2;			
RA	Waterston R.;			
RL	Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.			
CC	-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.			
DR	EMBL: U80836; AAC37893.1; -.			
DR	InterPro: IPR01841; Znf_finger.			
DR	Prfam: PR00097; zf-C3H4_1.			
DR	SMART: SM00184; RING_1.			
KW	Zinc-finger.			
SQ	SEQUENCE 425 AA; 48104 MW; 375F524E5C092B2D CRC64;			
RESULT	39			
ID	Q95QNG	PRELIMINARY;	PRT;	590 AA.
AC	Q95QNG			
DT	01-DEC-2001	(TREMBREL. 19, Created)		
DT	01-DEC-2001	(TREMBREL. 19, Last sequence update)		
DE	01-DEC-2001	(TREMBREL. 19, Last annotation update)		
GN	EBED8.16.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;			
OC	Rhabditidae; Peloderinae; Caenorhabditis.			
OX	NCBI_TAXID=6239;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BRISTOL N2;			
RX	MEDLINE=99059613; PubMed=9851916;			
RA	None;			
RT	"Genome sequence of the nematode <i>C. elegans</i> : a platform for investigating biology. The <i>C. elegans</i> sequencing Consortium.";			
RL	Science 282:2012-2018(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BRISTOL N2;			
RA	Chissoe S.;			
RT	"The sequence of <i>C. elegans</i> cosmid EBED8.;"			
RL	Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BRISTOL N2;			
RA	Waterston R.;			
RT	"Direct Submission."			
RT	Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.			
DR	EMBL: U33484; ARK93844.1; -.			
KW	Hypothetical protein.			
SQ	SEQUENCE 590 AA; 67414 MW; 56EA3FEEBD7D9CEB CRC64;			
Query Match	36.2%	Score 106; DB 5; Length 425;		
Best Local Similarity	40.9%	Score 105; DB 5; Length 590;		
Matches	18;	Pred. No. 3.6e-06; 7; Mismatches 17; Indels 2;	Gaps 1;	
Qy	4	CRICSDFFDHSDRVAIHCGHFTFLQCLIQWETAPSRTCPCCR 47		
Dp	1:1 : : : : : : : : :			
Dp	192	CSICFEDIKQNDKMSIAVGHTYHGCISQWIAIT-KROCPSCR 233		
RESULT	38			
QMAIL	QMAIL	PRELIMINARY;	PRT;	524 AA.
AC	QMAIL			
DT	01-OCT-2000	(TREMBREL. 15, Created)		
DT	01-OCT-2000	(TREMBREL. 15, Last sequence update)		
DT	01-DEC-2001	(TREMBREL. 19, Last annotation update)		
DE	F12M16.10			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			

RESULT	40	DR	HSSP; P28890; ICHC.
ID	O9VG16	DR	flyBase; FBgn0037944; CG6923.
AC	O9VG16;	DR	InterPro; IPR001841; Znf_fing.
DT	01-MAY-2000 (TREMBLrel. 13, Created)	DR	PFam; PF00097; zf-CHC4; 1.
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	DR	SMART; SM00184; RING; 1.
DE	CG6923 PROTEIN (LD2271P)	DR	Zinc-finger.
GN	CG6923.	KW	SEQUENCE 1256 AA; 138666 MW; 17FA760165507E4E CRC64;
OS	Drosophila melanogaster (Fruit fly).	DR	SEARCH completed: September 4, 2002, 16:16:09
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	Job time:	1493 sec
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	Qy	4 CTICSDFFDHSRDVAIHCHTFHQCCLQWFETAPSRCPCQRIQ 50
OC	Ephydriidae; Drosophilidae; Drosophila;	Matches	17; Conservative 9; Mismatches 19; Indels 1
OX	NCBI-Taxide7227;	Db	1187 CAICLNLFIENEVRRLPICMHLFHTCVDOWLV--NKHCPICRVDI 123
RN	[1]	OY	: : : : : : : : : : :
RP	SEQUENCE FROM N.A.	DR	SEARCH completed: September 4, 2002, 16:16:09
RC	STRAN-BERKELEY;	Job time:	1493 sec
RX	MEDLINE=20196006; PUBMed=10731132;	Qy	4 CTICSDFFDHSRDVAIHCHTFHQCCLQWFETAPSRCPCQRIQ 50
RA	Adams M.D., Celinkin S.E., Holt R.A., Evans C.A., Gocayne J.D.,	Matches	17; Conservative 9; Mismatches 19; Indels 1
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,	DR	CAICLNLFIENEVRRLPICMHLFHTCVDOWLV--NKHCPICRVDI 123
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,	DR	Zinc-finger.
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,	DR	SEQUENCE 1256 AA; 138666 MW; 17FA760165507E4E CRC64;
RA	Brandon R.C., Rogers Y.-H.C., Blazquez R.G., Champe M., Pfeiffer B.D.,	DR	SEARCH completed: September 4, 2002, 16:16:09
RA	Wan K.H., Doyle C., Baxter A., Helt G., Nelson C.R., Miklos G.L.G.,	Job time:	1493 sec
RA	Abrial J.F., Agbayani A., An H.-J., Andrews P., Pannkoch C., Baldwin D.,	Qy	4 CTICSDFFDHSRDVAIHCHTFHQCCLQWFETAPSRCPCQRIQ 50
RA	Bailey R.M., Basu A., Bakendale J., Bayraktaroglu L., Beasley E.M.,	Matches	17; Conservative 9; Mismatches 19; Indels 1
RA	Beeson K.Y., Benos P.V., Berman B.P., Brandari D., Bolshakov S.,	DR	CAICLNLFIENEVRRLPICMHLFHTCVDOWLV--NKHCPICRVDI 123
RA	Borkovka D., Botchan M.R., Bouck P., Brokstein P., Brottier P.,	DR	Zinc-finger.
RA	Burttis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,	DR	SEQUENCE 1256 AA; 138666 MW; 17FA760165507E4E CRC64;
RA	Cherry J.M., Cowley S., Dahlke C., Davenport L.B., Davies P.,	DR	SEARCH completed: September 4, 2002, 16:16:09
RA	de Pablo B.M., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,	Job time:	1493 sec
RA	Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,	Qy	4 CTICSDFFDHSRDVAIHCHTFHQCCLQWFETAPSRCPCQRIQ 50
RA	Durbin R.K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,	Matches	17; Conservative 9; Mismatches 19; Indels 1
RA	Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,	DR	CAICLNLFIENEVRRLPICMHLFHTCVDOWLV--NKHCPICRVDI 123
RA	Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,	DR	Zinc-finger.
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,	DR	SEQUENCE 1256 AA; 138666 MW; 17FA760165507E4E CRC64;
RA	Houston K.A., Howland T.J., Wei M.H., Ibegnami C.,	DR	SEARCH completed: September 4, 2002, 16:16:09
RA	Jalali M., Kalish F., Kapoor G.H., Ke Z., Kenison J.A., Ketchum R.A.,	Job time:	1493 sec
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,	Qy	4 CTICSDFFDHSRDVAIHCHTFHQCCLQWFETAPSRCPCQRIQ 50
RA	Lasko P., Lei E., Levitus Y.A., Li J., Li Z., Liang Y., Lin X.,	Matches	17; Conservative 9; Mismatches 19; Indels 1
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,	DR	CAICLNLFIENEVRRLPICMHLFHTCVDOWLV--NKHCPICRVDI 123
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Mosleref A.,	DR	Zinc-finger.
RA	Mount S.M., Moy M., Murphy D.M., Muzny D.M., Nelson D.L.,	DR	SEQUENCE 1256 AA; 138666 MW; 17FA760165507E4E CRC64;
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,	DR	SEARCH completed: September 4, 2002, 16:16:09
RA	Palazzolo M., Pittman G.S., Pan S., Pollard J.J., Puri V., Reese M.G.,	Job time:	1493 sec
RA	Reinert K., Remington K., Saunderson R.D.C., Scheeler F., Shen H.,	Qy	4 CTICSDFFDHSRDVAIHCHTFHQCCLQWFETAPSRCPCQRIQ 50
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,	Matches	17; Conservative 9; Mismatches 19; Indels 1
RA	Spiers E., Spradling A.C., Stapleton M., Strong R., Sun E.,	DR	CAICLNLFIENEVRRLPICMHLFHTCVDOWLV--NKHCPICRVDI 123
RA	Svirskas R., Treator C., Turner R., Venter E., Wang A.H., Wang X.,	DR	Zinc-finger.
RA	Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,	DR	SEQUENCE 1256 AA; 138666 MW; 17FA760165507E4E CRC64;
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,	DR	SEARCH completed: September 4, 2002, 16:16:09
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,	Job time:	1493 sec
RA	Zheng X.H., Zhong F.N., Zhou X., Zhu S., Zhu X., Smith H.O.,	Qy	4 CTICSDFFDHSRDVAIHCHTFHQCCLQWFETAPSRCPCQRIQ 50
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,	Matches	17; Conservative 9; Mismatches 19; Indels 1
RA	"The genome sequence of Drosophila melanogaster,"	DR	CAICLNLFIENEVRRLPICMHLFHTCVDOWLV--NKHCPICRVDI 123
RL	Science 287:2185-2195 (2000).	DR	Zinc-finger.
RN	[2]	DR	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.	DR	SEARCH completed: September 4, 2002, 16:16:09
RC	STRAN-Y, CN BN SP;	Job time:	1493 sec
RA	Stapleton M., Brookstein P., Hong L., Agbayani A., Carlson J.,	Qy	4 CTICSDFFDHSRDVAIHCHTFHQCCLQWFETAPSRCPCQRIQ 50
RA	Champine M., Chavez C., Doisett V., Farfan D., Frise E., George R.,	Matches	17; Conservative 9; Mismatches 19; Indels 1
RA	Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mongalli C.J.,	DR	CAICLNLFIENEVRRLPICMHLFHTCVDOWLV--NKHCPICRVDI 123
RA	Nuno J., Paclob J., Paragas V., Park S., Phouanenavong S., Wan K.,	DR	Zinc-finger.
RA	Yu C., Lewis S.E., Rubin G.M., Celinkin S.,	DR	SEQUENCE 1256 AA; 138666 MW; 17FA760165507E4E CRC64;
RA	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.	DR	SEARCH completed: September 4, 2002, 16:16:09
CC	-1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.	Job time:	1493 sec
DR	EMBL: AE003692; AAFF4693_1; -;	Qy	4 CTICSDFFDHSRDVAIHCHTFHQCCLQWFETAPSRCPCQRIQ 50
DR	EMBL: AY058520; AAU13749_1; -;	Matches	17; Conservative 9; Mismatches 19; Indels 1

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